APPENDIX A

RESULT 1
S39842
enniatin synthetase - fungus (Fusarium scirpi)
C;Species: Fusarium scirpi
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 03-Nov-2000
C;Accession: S39842; S35906; S65363
R;Haese, A.
submitted to the EMBL Data Library, November 1992
A;Reference number: S39842
A;Accession: S39842
A;Molecule type: DNA
A;Residues: 1-3131 <HAE>
A;Cross-references: EMBL:Z18755; NID:g2729; PIDN:CAA79245.1; PID:g2730
R;Haese, A.; Schubert, M.; Herrmann, M.; Zocher, R.
Mol. Microbiol. 7, 905-914, 1993
A;Title: Molecular characterization of the enniatin synthetase gene encoding a multifunctional
enzyme catalysing N-methyldepsipeptide formation in Fusarium scirpi.
A;Reference number: S35906; MUID:93247491; PMID:8483420
A;Accession: S35906
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 499-1074;1572-1988;2423-2566 <HA2>
A;Cross-references: EMBL:Z18755
A;Experimental source: strain ETH 1536/J5
R;Pieper, R.; Haese, A.; Schroeder, W.; Zocher, R.
Eur. J. Biochem. 230, 119-126, 1995
A;Title: Arrangement of catalytic sites in the multifunctional enzyme enniatin synthetase.
A;Reference number: S65363; MUID:95324513; PMID:7601090
A;Accession: S65363
A;Molecule type: protein
A;Residues: 2029-2048;430-437;1011-1020;1021-1034;1677-1695;2294-2299 <PIE>
A;Experimental source: strain ETH 1536/J5
C;Genetics:
A;Gene: esyn1
C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
C;Keywords: carrier protein; multifunctional enzyme; phosphopantetheine; phosphoprotein
F;531-985/Domain: acetate-CoA ligase homology <ACL1>
F;1603-2100/Domain: acetate-CoA ligase homology <ACL2>
F;2507-2574/Domain: acyl carrier protein homology <ACP1>
F;2601-2667/Domain: acyl carrier protein homology <ACP2>
F;1047,2538,2632/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

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   Query Match              55.2%;  Score 9139;  DB 2;  Length 3131;
   Best Local Similarity    55.8%;  Pred. No. 0;
   Matches 1818;  Conservative  490;  Mismatches  758;  Indels  190;  Gaps  37;

Qy        8 PTMGVEQQALSLSCPLLPHDDEKHSDNLYEQATRHFGLSRDKIENVLPCTSFQCDVIDCA 67
            |: |  :  ||:          |  | || :|  || :|||||: | || |||||||
Db        6 PSDGQQDPALA------------SKTLCEQISRALGLGQDKIENIFPGTPFQRDVIDCA 52

Qy       68 VDDRRHAIGHVVYDIPNTVDIQRLAAAWKEVVRQTPILRTGIFTSETGDSFQIVLKEG-C 126
            ||:: |:|| |::||  :| ||||||||| | || ||| |||::|| |:||::
Db       53 ADDKQRAVGHAVFEIPKDIDAARLAAAWKETVLHTPALRTCTFTSKSGDVLQVVLRDSFV 112

Qy      127 LPWMYATCLGMKGAVIQDEAVAAMTGPRCNRYVVLEDPSTKQRLLIWTFSHALVDYTVQE 186
            ||      : :| ||:||||  ||: |||||:|:||| ||:| |||||||||| | ||
Db      113 FSWMSGPSVDLKEAVVQDEAAAALAGPRCNRFVLLEDPDTKERQLIWTFSHALVDSTFQE 172

Qy      187 RILQRVLTVY-DGRD------------------------VECPRIKDTEHVSRFWQQ 218
            |||:|||  | |  |                        ::  |:  |  :   ||:
Db      173 RILRRVLKAYKDANDEHPRQFETPDSSQATPEEDLQPNPSKMLKIPQAADMDRAVEFWKD 232

Qy      219 HFEGLDASVFPLLPSHLTVCNPNARAEHHISYTGPVQRKWSHTSICRAALAVLLSRFTHS 278
            |  ||      |          :|:|:|||  |||:  |:| |  :||| |||:|||||:|||
Db      233 HLSGLKCFCLPAFVLSSVYAHPDAKAEHRISYSSSAQQKMSSATICRTALAILLSRYTHS 292
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Qy    279 SEALFGVVTEQSHNSEDQRRSIDGPARTVVPIRVLCAPDQYVSDVIGAITAHEHAMRGFE 338
          |||||:||||:     |:|    :||| |||||||||| || :| |||::  | ::: ||| |
Db    293 PEALFGIVTEQTPLLEEQ-LMLDGPTRTVVPIRVSCASEQSVSDIMSTIDSYDQTMRQFA 351

Qy    339 HAGLRNIRRTGDDGSAACGFQTVLLVTDGDAPKTPGSVL----HRSVEESDRFMPCANRA 394
          |||||||    ||| |||||| :        :|| |     | || : |:|| |||
Db    352 HAGLRNIASAGDDESAACGSRPF----SWSQMETPSQHLLGKFSRKTEEPEGFIPCTNRA 407

Qy    395 LLLDCQMAGNSASLVARYDHNVIDPRQMSRFLRQLGYLIQQFHHHVDLPLVKELDVVTAE 454
          ||| |||   : | |||| ::|| ||:| |||||:||| :    | |:::|::| |
Db    408 LLLSCQMTSSGAHLTARYDQSIIDAEQMARLLRQLGHLIQNLPNLHRSP-VEKVDMMTQE 466

Qy    455 DCAEIEKWNSERLTMQDALIHDTISKWAAGDPNKAAVFAWDGEWTYAELDNISSRLAVYI 514
          |  |||:|||: :  || |||  : || :  ||||||| |||||||||||||||:||||| :|
Db    467 DWLEIERWNSDSIDAQDTLIHSEMLKWTSQSPNKAAVAAWDGEWTYAELDNVSSRLAQHI 526

Qy    515 QSLDLRPGQAILPLCFEKSKWVVATILAVLKVGRAFTLIDPCDPSARMAQVCQQTSATVA 574
          |:||   ||:|: |||||||||||::|||||| | |||||||| || || ||||||||||
Db    527 NSIDLGKEHAIVPIYFEKSKWVVASMLAVLKAGHAFTLIDPSDPPARTAQVVQQTSATVA 586

Qy    575 LTSKLHNTTLRSVVSRCIVVDDDLLRSLPHADGRLKATVKPQDLAYVIFTSGSTGEPKGI 634
          ||||||    |::| | |||||||:: ::|||  :   | |:|| |||||||||||||| ||||
Db    587 LTSKLHRETVQSTVGRCIVVDEEFVKSLPQS-SELSASVKAHDLAYVIFTSGSTGIPKGI 645

Qy    635 MIEHRGFVSCAMKFGPALGMDEHTRALQFASYAFGACLVEVVTALMHGGCVCIPSDDDRL 694
          ||||| | |||:||||||| |      ||||||| |:||||||::|::| |:||||||||||||||||:
Db    646 MIEHRSFSSCAIKFGPALGITSDTRALQFGSHAFGACILEIMTTLIHGGCVCIPSDDDRM 705

Qy    695 NNVPEFIKRAQVNWVILTPSYIGTFQPEDVPGLQTLVLVGEPISASIRDTWASQVRLLNA 754
          ||| ||| |  |    |||:|||||| ||||:||||||| |||||:|||: : || :|:|||
Db    706 NNVLEFINRTNVQLGHATPSYMGTFQPEVVPGLKTLVLVGEQMSASVNEVWAPRVQLLNG 765

Qy    755 YGQSESSTMCSVTEVSPLSLEPNNIGRAVGARSWIIDPDEPDRLAPIGCIGELVIESPGI 814
          |||||||::|  | ::||  |  |||||||  |||| |||:||:::|:|||||| :||||||| ||
Db    766 YGQSESSSICCVAKISPGSSEPNNIGHAVGAHSWIVDPEDPNRLAPIGAVGELVIESAGI 825

Qy    815 ARDYIIAPPPDKSPFLLAPPAWYPAGKLSNAFKFYKTGDLVRYGPDGTIVCLGRKDSQVK 874
          |||||:||   ||||:      | |||| :|  : ||  |:|||  | ||:|||||| ||||
Db    826 ARDYIVAPTQDKSPFIKTAPTWYPAKQLPDGFKIYRTGDLACYASDGSIVCLGRMDSQVK 885

Qy    875 IRGQRVEISAVEASLRRQLPSDIMPVAEAIKRSDSSGSTVLTAFLIGSSKSGDGNGHALS 934
          |||||||: ||| ||:|:| |:   | ||:| |||| :|||||||||   :|: | |
Db    886 IRGQRVELGAVETHLRQQMPDDMTIVVEAVKFSDSSSTTVLTAFLIG---AGEKNSH--- 939

Qy    935 AADAVILDHGATNEINAKLQQILPQHSVPSYYIHMENLPRTATGKADRKMLRSIASKLLG 994
              ||| || |||||||::|:||:||:|:::|| | |||:||||| |: | ||:| |
Db    940 -----ILDQRATREINAKMEQVLPRHSIPAFYISMNNLPQTATGKVDRRKLRIMGSKILS 994

Qy    995 ELSQNVTSQPIEKHDAPATGIEVKLKELWFLSLNLNPNSQDVGASFFDLGGNSIIAIKMV 1054
          : : :  ||  :    : |   ||: :| ||:| | |  :: |:||::|||||||||||||||
Db    995 QKTHSTPSQQSQAAISSGTDTYTKLESIWITSLDLGPGSANMSATFFEMGGNSIIAIKMV 1054

Qy   1055 NMARSAGIALKVSDIFQNPTLAGLVDVIGRDPAPYNLIPTTAYSGPV-EQSFAQGRLWFL 1113
          ||||| || |||||:|||||||||:|||||||| ::        ||:||| ||| |||:|| |:|||
Db   1055 NMARSNGIELKVSDIYQNPTLAGLKAIVIGTSLPYSLIPKVTRQGPVSEQSYAQNRMWFL 1114

Qy   1114 DQIELDALWYLLPYAVRMRGPLHIDALTIALLAIQQRHETLRTTFEEQDGVGVQVVHASP 1173
          ||:   | |||:|:|||||||: :|||| ||||::::||||||||||::||||||| |||||::|
Db   1115 DQLSEGASWYLIPFAVRMRGPVDVDALTRALLALEQRHETLRTTFENQDGVGVQIIHDRL 1174

Qy   1174 ISDLRIID-VSGDRNSDYLQLLHQEQTTPFILACQAGWRVSLIRLGEDDHILSIVMHHII 1232
           :|::||  : ||      |: |:: :|| | :     :||| :||||||:||||||||||||||||
Db   1175 SKELQVIDALDGDEGG--LKTLYKVETTTFDITSEAGWSSTLIRLGKDDHILSIVMHHII 1232

Qy   1233 SDGWSIDILRRELSNFYSAALRGSDPLSVVSPLPLHYRDFSVWQKQVEQETEHERQLEYW 1292
          |||||||:||||| |:|||:| || ||  :|||: |: ||:||||||  | |||||||:||
Db   1233 SDGWSIDVLRRELIQLYAAALQGKDPSSALTPLPIQYSDFAVWQKQEAQAAEHERQLQYW 1292
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Qy   1293 VKQLADSSAAEFLTDFPRPNILSGEAGSVPVTIEGELYERLQEFCKVEQMTPFAVLLGAF 1352
          |||||||  |:  ||||||::|||:||  |||  |:||||::|:  ||      |  |::|| ||
Db   1293 KKQLADSSPAKIPTDFPRPDLLSGDAGVVPVAIDGELYQKLRGFCNKHNSTAFSILLAAF 1352

Qy   1353 RATHYRLTGAEDSIIGTPIANRNRQELENMIGFFVNTQCMRITVDGDDTFESLVRQVRTT 1412
          || ||||||  :|::||  ||||||| |||||||||||||||  ||||||||||||||:|
Db   1353 RAAHYRLTAVDDAVIGIPIANRNRWELENMIGFFVNTQCMRIAVDETDTFESLVRQVRST 1412

Qy   1413 ATAAFEHQDVPFERVVTALLPRSRDLSRNPLAQLTFALHSQQDLGKFELEGLVAEPVSNK 1472
          ||||  |:||||||||:||  |    ||||| ||||:  ||:|||:|||:|||||   :||:::|
Db   1413 TTAAFAHEDVPFERVVSALQPGHRDLSRTPLAQIMFAVHSQKDLGRFELEGIQSEPIASK 1472

Qy   1473 VYTRFDVEFHLFQEAGRLSGNVAFAADLFKPETISNVVAIFFQILRQGIRQPRTPIAVLP 1532
          ||||||||||||:|  | |:  ||  |||||||||| |||::||||||| |:  || |  |:|||
Db   1473 AYTRFDVEFHLFQQADGLKGSCNFATDLFKPETIQNVVSVFFQILRHGLDQPETCISVLP 1532

Qy   1533 LTDGLADLRAMGLLEIEKAEYPRESSVVDVFRKQVAAHPHAFAVVDSASRLTYADLDRQS 1592
          ||||:  :||  :  ||||::  |||:|||||||:| ||:|  || ||:||||||||:||  :|
Db   1533 LTDGVEELRRLDLLEIKRTNYPRDSSVVDVFREQAAANPEVIAVTDSSSRLTYAELDNKS 1592

Qy   1593 DQLATWLGRRNMTAETLVGVLAPRSCQTVVAILGILKANLAYLPLDVNCPTARLQTILST 1652
          :  |:  ||  |||:|  |||| |||||||||:|:||  :|||||||||||||||  |  |::  |||:
Db   1593 ELLSRWLRRRNLTPETLVSVLAPRSCETIVAYVGILKANLAYLPLDVRSPVTRMKDILSS 1652

Qy   1653 LNRHKLVLLGSNATTPDVQIPDVELVRISDILDRPINGQAKLNGHTKSNGYSKPNGYTHL 1712
          ::  :  :||:||       |   :|  :||||||:|     |    |
Db   1653 VSGNTIVLMGSGVEDPGFDLPQLELVRITDTFDETI------------------------ 1688

Qy   1713 KGYSNLNGYSKQNGYAQLNGHRERNNYLDLNGHSLLNGNSDITTS-GPSATSLAYVIFTS 1771
                                                       |:  |   |||||||||:|||
Db   1689 ------------------------------------EDVQDSPQPSATSLAYVVFTS 1709

Qy   1772 GSTGKPKGVMVEHRSIIRLAKKNRIISRFPSVAKVAHLSNIAFDAATWEMFAALLNGGTL 1831
          |||||||||||:|||:|||:|:||  | |:         |||  |::::: | ||| | ||:   ||||||:
Db   1710 GSTGKPKGVMIEHRAIVRLVKSDN-FPGFPSPARMSNVFNPAFDGAIWEINWMLLNGGTV 1768

Qy   1832 VCIDYMTTLDSKTLEAAFAREQINAALLTPALLKQCLANIPTTLGRLSALVIGGDRLDGQ 1891
          |||||:||||  |  |  ||:|::|||  ||:||  |  :   |   |   |::||:|  |   :
Db   1769 VCIDYLTTLDGKELAAVFAKERVNAAFFAPAMLKLYLVDAREALKNLDFLIVGGERFDTK 1828

Qy   1892 DAIAAHALVGAGVYNAYGPTENGVISTIYNITKNDSFINGVPIGCAISNSGAYITDPDQQ 1951
          :|:  |    ||    :  |  |||||| |:|||  |||  |:::::  |||||||  :|  ||||||:  ||:||
Db   1829 EAVEAMPLVRGKIANIYGPTEAGIISTCYNIPKDEAYTNGVPIGGSIYNSGAYVMDPNQQ 1888

Qy   1952 LVPPGVMGELVVTGDGLARGYTDPALDAGRFVQIMINDKAVRAYRTGDRARYRVGDGQIE 2011
          || |||||||||||||: ||||:| |:  ||: |  |  |   |  :|||||||| |  ||||| :|
Db   1889 LVGLGVMGELVVTGDGVGRGYTNPELNKNRFIDITIEGKTFKAYRTGDRMRARVGDGLLE 1948

Qy   2012 FFGRMDQQVKIRGHRIEPAEVERAILDQDSARDAVVVIRHQEGEEPEMVGFVATHGDHSA 2071
          ||||||  |  ||||:|||  |||  |:|   :  :||:|: | :|  :|       | |:
Db   1949 FFGRMDNQFKIRGNRIEAGEVESAMLSLKNVLNAAIVVAGAE----KMKGH-SRWSDSSS 2003

Qy   2072 --------EQEEADDQVEGWKDFFESNTYADMDT-IGQSAIGNDFTGWTSMYDGSEINKA 2122
                  ::         ::       | |||   |:|:  |  :  |||||||||  |||||||||   :|:|
Db   2004 RTTRMIPRRRKRQATKLRAGMDHFESGMYSDISTAVDQSAIGNDFKGWTSMYDGKDIDKG 2063

Qy   2123 EMQEWLDDTMRTLLDGQAPGHVLEIGTGSGMVLFNLGAGLQSYVGLEPSRSAATFVTKAI 2182
          |||||||| :  || :|| |  |||||||||||:||||  || |||||:||:|| || :|:
Db   2064 EMQEWLDDAIHTLHNGQIPRDVLEIGTGSGMILFNLNPGLNSYVGLDPSKSAVEFVNRAV 2123

Qy   2183 NSTPALAGKAEVHVGTATDINRLRGLRPDLVVLNSVVQYFPTPEYLLEVVESLVRIPGVK 2242
          |:|  ||||:|||| |||:||| ||:|:|  :  |||||  |||||||||||||||||||  ||::  |:  || ||
Db   2124 ESSPKFAGKAKVHVGMATDVNKLGEVHPDLVVFNSVVQYFPTPEYLAEVIDGLIAIPSVK 2183

Qy   2243 RVVFGDIRSHATNRHFLAARALHSLG--SKATKDAIRQKMTEMEEREEELLVDPAFFTAL 2300
          |:  |||||:|||  ||||||||:|:||   :  ||||  :|||  |:|:|||||  ||:||||||  |
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Db   2184 RIFLGDIRSYATNGHFLAARAIHTLGTNNNATKDRVRQKIQELEDREEEFLVEPAFFTTL 2243

Qy   2301 LQGQLADRIKHVEILPKNMRATNELSAYRYTAVIHVRGPEEQSRPVYPIQVNDWIDFQAS 2360
          : :  | :|||||:|||:|||||||||||||:|:|  :|  ||| |: : |:||:|
Db   2244 KE-RRPDVVKHVEIIPKNMKATNELSAYRYTAVVHLR--DETDEPVYHIEKDSWVDFEAK 2300

Qy   2361 RIDRRALLRLLQRSADAATVAVSNIPYSKTIVERHVVESLDNNNRENTHRAPDGAAWISA 2420
          ::|: |||  |: | || :||||| |: |  || :|||| :::::| |||||:||
Db   2301 QMDKTALLDHLRLSKDAMSVAVSNITYAHTAFERRIVESLDEDSKDDTKGTLDGAAWLSA 2360

Qy   2421 VRSKAERCTSLSVTDLVQLGEEAGFRVEVSAARQWSQSGALDAVFHRYNLPTQSNSRVLI 2480
          |||:||   ||:| |:::: :|||||||||||||||||||| ||  : | | | ||
Db   2361 VRSEAENRASLTVPDILEIAKEAGFRVEVSAARQWSQSGALDAAFHHF--PPSSTDRTLI 2418

Qy   2481 QFPTEDGQTRRSATLTNRPLQRLQSRRFASQIREQLKAVLPSYMIPSRIVVIDQMPLNAN 2540
          |||| | : | || |||||:|| | |:||:|: ::||||:| |||:| |||:|
Db   2419 QFPT-DNELRSSLTLANRPLQKLQRRRAALQVREKLQTLVPSYMVPPNIVVLDTMPLNTN 2477

Qy   2541 GKVDRKELTRRAQIAPKSQAAPAKPVKQVD-PFVNLEAILCEEFAEVLGMEVGVNDHFFQ 2599
          ||:||||||||: || | | | | ||  :| |||| || ||:| ::|||||
Db   2478 GKIDRKELTRRARTLPKQQTAAPVP----DFPISDIEITLCEEATEVFGMKVEISDHFFQ 2533

Qy   2600 LGGHSLLATKLVARLSRRLNGRVSVRDVFDQPVISDLAVTLRQGLTLENAIPATPDSGYW 2659
          |||||||||||:::|: ||: ||:|:|||| || :|||| :|||| ::| :    | |
Db   2534 LGGHSLLATKLISRIQHRLHVRVTVKDVFDSPVFADLAVIIRQGLAMQNPVAEGQDKQGW 2593

Qy   2660 EQTMSAPTTPSDDMEAVLCKEFADVLGVEVSATDSFFDLGGHSLMATKLAARISRRLDVP 2719
          |:  |  ::| :||:||| ||| || ||:||||||||||||||||| || |||
Db   2594 ----SSRVAPRTEVEKMLCEEFAAGLGVPVGITDNFFDLGGHSLMATKLAVRIGRRL--- 2646

Qy   2720 VSIKDIFDHS-------VPLNLARKIRLTQAKGHEAT-NGVQIANDAPFQLISVEDPEIF 2771
          |  ||         ||:|: : :| :| : : :|:|  |||| :|||| |
Db   2647 -----IRHHSQGHLRLPCAFQLAKKLESSHSKSYEESGDDIQMADYTAFQLLDLEDPQDF 2701

Qy   2772 VQREIAPQLQCSPETILDVYPATQMQRVFLLNPVTGKPRSPTPFHIDFPPDADCASLMRA 2831
          || :|| |||   || |||:||||:| || | :| ||:| ||:|  :|
Db   2702 VQSQIRPQLDSCYGTIQDVYPSTQMQKAFLFDPTTGEPRGLVPFYIDFPSNADAETLTKA 2761

Qy   2832 CASLAKHFDIFRTVFLEARGELYQVVLKHVDVPIEMLQTEENINSATRSFLDVDAEKPIR 2891
          :|  |:|||||||| |:|||||::|:::||  ::||:|:|:|| :||| : |:|
Db   2762 IGALVDKLDMFRTVFLEAAGDLYQVVVEHLNLPIETIETEKNVNTATGDYLDVHGKDPVR 2821

Qy   2892 LGQPLIRIAILEKPGSTLRVILRLSHALYDGLSLEHILHSLHILFFGGSLPPPPKFAGYM 2951
          || | |: ||| |  |::||:||:|||||||||| |:|:  ||:| | :||||  :|| ||
Db   2822 LGHPCIQFAIL-KTASSVRVLLRMSHALYDGLSFEYIVRGLHVLYSGRNLPPPTQFARYM 2880

Qy   2952 QHVASSRREGYDFWRSVLRDSSMTVIKGNNNTTPPPPPQQQSTPSGAHHASKVVTIPTQA 3011
          |: | || ||| |||::: |||: ||  :|:  | | |  :| ||
Db   2881 QYAAHSREEGYPFWREVLQNAPMTVLHDTNNGM----SEQEMPASKAVHLSEVVNVPAQA 2936

Qy   3012 NTDSRITRATIFTTACALMLAKEDNSSDVVFGRTVSGRQGLPLAHQNVIGPCLNQVPVRA 3071
          :|  |:||:| |||||:|||| | |||||||||: |:||||:  |:: |||| | |||  |
Db   2937 IRNSTNTQATVFNTACALVLAKESGSQDVVFGRIVSGRQGLPVVWQDIIGPCTNAVPVHA 2996

Qy   3072 RGLNRGTTHHRELLREMQEQYLNSLAFETLGYDEIKAHCTDWPDVPATASFGCCIVYQNF 3131
          | :: | : :  ::|:::|||| :| ||:||::|||  :|||||:     :| |: | ||
Db   2997 R-VDDG--NPQRIIRDLRDQYLRTLPFESLGFEEIKRNCTDWPE--ELTNFSVCVTYHNF 3051

Qy   3132 DSHPDSRVEEQRLQIGVLSRNYEAINEGLVHDLVIAGESEPDGDDLRVTVVANRRLCDEE 3191
          : ||:| |: |:::|||:: |    ::|| |||| | || :|:|||||  || :|
Db   3052 EYHPESEVDNQKVEMGVLAKYVELSENEPLYDLAIAGEVEADGVNLKVTVVAKARLYNEA 3111

Qy   3192 RLKRMLEELCGNIRAL 3207
          |:: :|||:|    |
Db   3112 RIRHVLEEVCKTFNGL 3127
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